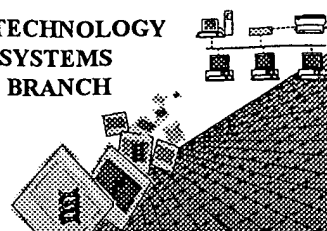


BIOTECHNOLOGY
SYSTEMS
BRANCH



0590-04D0
02/12/02

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/045,400
Source: 0116
Date Processed by STIC: 2/5/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/245,400
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



OIPE

RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/10/045,400

TIME: 17:06:00

Input Set : A:\ES.txt

Output Set: N:\CRF3\02052002\J045400.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Moon, Chulso
4 Mao, Li
6 <120> TITLE OF INVENTION: Dap-Kinase and Hoxa9, Two Human Genes Associated With
Genesis,
7 Progression, and Aggressiveness of Non-Small Cell Lung Cancer
9 <130> FILE REFERENCE: 10620-1U1
OK 11 <140> CURRENT APPLICATION NUMBER: US/10/045,400
12 <141> CURRENT FILING DATE: 2001-11-29
14 <150> PRIOR APPLICATION NUMBER: US 60/250,083
15 <151> PRIOR FILING DATE: 2000-11-29
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 20
23 <212> TYPE: DNA
C--> 24 <213> ORGANISM: Artificial/Unknown *invalid - see item 10 on Eva Summary Sheet*
26 <220> FEATURE:
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28 <222> LOCATION: (1)..(20)
29 <223> OTHER INFORMATION: HoxA9 PCR Primer
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37 <211> LENGTH: 20
38 <212> TYPE: DNA
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43 <222> LOCATION: (1)..(20)
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67 aaaacaaccc agcgaaggcg ccttctccga aaacaatgcc gagaatgaga gcggcggaga 180

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86 ctccctagct gtgttcccg cgcgcgcccg gctagtctcc ggcgtggcg cctatggctg 180
88 gcctccgaca gcgctccgga gggaccggg gagctcccag gcgcccggga ctggagactg 240
90 atgcatgagg ggcctacgga ggcgcaggag cgggtggtgat ggtctgggaa gcggagctga 300
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93 Met Thr Val Phe Arg Gln
94 1 5
96 gaa aac gtg gat gat tac tac gac acc ggc gag gaa ctt ggc agt gga 402
97 Glu Asn Val Asp Asp Tyr Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly
98 10 15 20
100 cag ttt gcg gtt gtg aag aaa tgc cgt gag aaa agt acc ggc ctc cag 450
101 Gln Phe Ala Val Val Lys Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln
102 25 30 35
104 tat gcc gcc aaa ttc atc aag aaa agg agg act aag tcc agc cgg cgg 498
105 Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg
106 40 45 50
108 ggt gtg agc cgc gag gac atc gag cgg gag gtc agc atc ctg aag gag 546
109 Gly Val Ser Arg Glu Asp Ile Glu Arg Glu Val Ser Ile Leu Lys Glu
110 55 60 65 70
112 atc cag cac ccc aat gtc atc acc ctg cac gag gtc tat gag aac aag 594
113 Ile Gln His Pro Asn Val Ile Thr Leu His Glu Val Tyr Glu Asn Lys
114 75 80 85
116 acg gac gtc atc ctg atc ttg gaa ctc gtt gca ggt ggc gag ctg ttt 642
117 Thr Asp Val Ile Leu Ile Leu Glu Leu Val Ala Gly Gly Glu Leu Phe
118 90 95 100
120 gac ttc tta gct gaa aag gaa tct tta act gaa gag gaa gca act gaa 690
121 Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr Glu Glu Glu Ala Thr Glu
122 105 110 115
124 ttt ctc aaa caa att ctt aat ggt gtt tac tac ctg cac tcc ctt caa 738
125 Phe Leu Lys Gln Ile Leu Asn Gly Val Tyr Tyr Leu His Ser Leu Gln
126 120 125 130
128 atc gcc cac ttt gat ctt aag cct gag aac ata atg ctt ttg gat aga 786
129 Ile Ala His Phe Asp Leu Lys Pro Glu Asn Ile Met Leu Leu Asp Arg
130 135 140 145 150
132 aat gtc ccc aaa cct cgg atc aag atc att gac ttt ggg ttg gcc cat 834
133 Asn Val Pro Lys Pro Arg Ile Lys Ile Ile Asp Phe Gly Leu Ala His
134 155 160 165
136 aaa att gac ttt gga aat gaa ttt aaa aac ata ttt ggg act cca gag 882
137 Lys Ile Asp Phe Gly Asn Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/045,400

DATE: 02/05/2002

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Output Set: N:\CRF3\02052002\J045400.raw

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142		185		190		195		
144	gat atg tgg agt atc ggg gta ata acc tat atc ctc cta agt ggg gcc							978
145	Asp Met Trp Ser Ile Gly Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala							
146		200		205		210		
148	tcc cca ttt ctt gga gac act aag caa gaa acg tta gca aat gta tcc							1026
149	Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Val Ser							
150	215		220		225		230	
152	gct gtc aac tac gaa ttt gag gat gaa tac ttc agt aat acc agt gcc							1074
153	Ala Val Asn Tyr Glu Phe Glu Asp Glu Tyr Phe Ser Asn Thr Ser Ala							
154		235		240		245		
156	cta gcc aaa gat ttc ata aga aga ctt ctg gtc aag gat cca aag aag							1122
157	Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu Val Lys Asp Pro Lys Lys							
158		250		255		260		
160	aga atg aca att caa gat agt ttg cag cat ccc tgg atc aag cct aaa							1170
161	Arg Met Thr Ile Gln Asp Ser Leu Gln His Pro Trp Ile Lys Pro Lys							
162		265		270		275		
164	gat aca caa cag gca ctt agt aga aaa gca tca gca gta aac atg gag							1218
165	Asp Thr Gln Gln Ala Leu Ser Arg Lys Ala Ser Ala Val Asn Met Glu							
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168	aaa ttc aag aag ttt gca gcc cgg aaa aaa tgg aaa caa tcc gtt cgc							1266
169	Lys Phe Lys Lys Phe Ala Ala Arg Lys Lys Trp Lys Gln Ser Val Arg							
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172	ttg ata tca ctg tgc caa aga tta tcc agg tca ttc ctg tcc aga agt							1314
173	Leu Ile Ser Leu Cys Gln Arg Leu Ser Arg Ser Phe Leu Ser Arg Ser							
174		315		320		325		
176	aac atg agt gtt gcc aga agc gat gat act ctg gat gag gaa gac tcc							1362
177	Asn Met Ser Val Ala Arg Ser Asp Thr Leu Asp Glu Glu Asp Ser							
178		330		335		340		
180	ttt gtg atg aaa gcc atc atc cat gcc atc aac gat gac aat gtc cca							1410
181	Phe Val Met Lys Ala Ile Ile His Ala Ile Asn Asp Asp Asn Val Pro							
182		345		350		355		
184	ggc ctg cag cac ctt ctg ggc tca tta tcc aac tat gat gtt aac caa							1458
185	Gly Leu Gln His Leu Leu Gly Ser Leu Ser Asn Tyr Asp Val Asn Gln							
186		360		365		370		
188	ccc aac aag cac ggg aca cct cca tta ctc att gct gct ggc tgt ggg							1506
189	Pro Asn Lys His Gly Thr Pro Pro Leu Leu Ile Ala Ala Gly Cys Gly							
190	375		380		385		390	
192	aat att caa ata cta cag ttg ctc att aaa aga ggc tcg aga atc gat							1554
193	Asn Ile Gln Ile Leu Gln Leu Leu Ile Lys Arg Gly Ser Arg Ile Asp							
194		395		400		405		
196	gtc cag gat aag ggc ggg tcc aat gcc gtc tac tgg gct gct cgg cat							1602
197	Val Gln Asp Lys Gly Gly Ser Asn Ala Val Tyr Trp Ala Ala Arg His							
198		410		415		420		
200	ggc cac gtc gat acc ttg aaa ttt ctc agt gag aac aaa tgc cct ttg							1650
201	Gly His Val Asp Thr Leu Lys Phe Leu Ser Glu Asn Lys Cys Pro Leu							
202		425		430		435		

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206		440					445					450					
208	tat	ggc	cat	gct	gac	gtg	gct	caa	gtt	act	tgt	gca	gct	tcg	gct	caa	1746
209	Tyr	Gly	His	Ala	Asp	Val	Ala	Gln	Val	Thr	Cys	Ala	Ala	Ser	Ala	Gln	
210	455					460					465					470	
212	atc	cca	ata	tcc	agg	aca	aag	gaa	gaa	gaa	acc	ccc	ctg	cac	tgt	gct	1794
213	Ile	Pro	Ile	Ser	Arg	Thr	Lys	Glu	Glu	Glu	Thr	Pro	Leu	His	Cys	Ala	
214					475					480					485		
216	gct	tgg	cac	ggc	tat	tac	tct	gtg	gcc	aaa	gcc	ctt	tgt	gaa	gcc	ggc	1842
217	Ala	Trp	His	Gly	Tyr	Tyr	Ser	Val	Ala	Lys	Ala	Leu	Cys	Glu	Ala	Gly	
218			490						495				500				
220	tgt	aac	gtg	aac	atc	aag	aac	cga	gaa	gga	gag	acg	ccc	ctc	ctg	aca	1890
221	Cys	Asn	Val	Asn	Ile	Lys	Asn	Arg	Glu	Gly	Glu	Thr	Pro	Leu	Leu	Thr	
222		505					510					515					
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226		520				525					530						
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229	Gly	Ala	Asp	Leu	Asn	Ala	Cys	Asp	Lys	Asp	Gly	His	Ile	Ala	Leu	His	
230	535				540					545					550		
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233	Leu	Ala	Val	Arg	Arg	Cys	Gln	Met	Glu	Val	Ile	Lys	Thr	Leu	Leu	Ser	
234					555				560						565		
236	caa	ggg	tgt	ttc	gtc	gat	tat	caa	gac	agg	cac	ggc	aat	act	ccc	ctc	2082
237	Gln	Gly	Cys	Phe	Val	Asp	Tyr	Gln	Asp	Arg	His	Gly	Asn	Thr	Pro	Leu	
238			570						575				580				
240	cat	gtg	gca	tgt	aaa	gat	ggc	aac	atg	cct	atc	gtg	gtg	gcc	ctc	tgt	2130
241	His	Val	Ala	Cys	Lys	Asp	Gly	Asn	Met	Pro	Ile	Val	Val	Ala	Leu	Cys	
242		585					590					595					
244	gaa	gca	aac	tgc	aat	ttg	gac	atc	tcc	aac	aag	tat	ggg	cga	acg	cct	2178
245	Glu	Ala	Asn	Cys	Asn	Leu	Asp	Ile	Ser	Asn	Lys	Tyr	Gly	Arg	Thr	Pro	
246		600				605					610						
248	ctg	cac	ctt	gcg	gcc	aac	aac	gga	atc	cta	gac	gtg	gtc	cgg	tat	ctc	2226
249	Leu	His	Leu	Ala	Ala	Asn	Asn	Gly	Ile	Leu	Asp	Val	Val	Arg	Tyr	Leu	
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257	Ala	Glu	Asp	Leu	Ala	Arg	Ser	Glu	Gln	His	Glu	His	Val	Ala	Gly	Leu	
258			650						655				660				
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261	Leu	Ala	Arg	Leu	Arg	Lys	Asp	Thr	His	Arg	Gly	Leu	Phe	Ile	Gln	Gln	
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265	Leu	Arg	Pro	Thr	Gln	Asn	Leu	Gln	Pro	Arg	Ile	Lys	Leu	Lys	Leu	Phe	
266		680				685						690					
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/045,400

DATE: 02/05/2002

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Output Set: N:\CRF3\02052002\J045400.raw

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273	Gly	Leu	Leu	Arg	Ser	Phe	Phe	Arg	Arg	Arg	Arg	Pro	Arg	Leu	Ser	Ser	
274					715					720					725		
276	acc	aac	tcc	agc	agg	ttc	cca	cct	tca	ccc	ctg	gct	tct	aag	ccc	aca	2562
277	Thr	Asn	Ser	Ser	Arg	Phe	Pro	Pro	Ser	Pro	Leu	Ala	Ser	Lys	Pro	Thr	
278				730					735					740			
280	gtc	tca	gtg	agc	atc	aac	aac	ctg	tac	cca	ggc	tgc	gag	aac	gtg	agt	2610
281	Val	Ser	Val	Ser	Ile	Asn	Asn	Leu	Tyr	Pro	Gly	Cys	Glu	Asn	Val	Ser	
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284	gtg	agg	agc	cgc	agc	atg	atg	ttc	gag	ccg	ggt	ctt	acc	aaa	ggg	atg	2658
285	Val	Arg	Ser	Arg	Ser	Met	Met	Phe	Glu	Pro	Gly	Leu	Thr	Lys	Gly	Met	
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289	Leu	Glu	Val	Phe	Val	Ala	Pro	Thr	His	His	Pro	His	Cys	Ser	Ala	Asp	
290	775				780						785				790		
292	gac	cag	tcc	acc	aag	gcc	atc	gac	atc	cag	aac	gct	tat	ttg	aat	gga	2754
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294				795						800					805		
296	gtt	ggc	gat	ttc	agc	gtg	tgg	gag	ttc	tct	gga	aat	cct	gtg	tat	ttc	2802
297	Val	Gly	Asp	Phe	Ser	Val	Trp	Glu	Phe	Ser	Gly	Asn	Pro	Val	Tyr	Phe	
298			810					815				820					
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301	Cys	Cys	Tyr	Asp	Tyr	Phe	Ala	Ala	Asn	Asp	Pro	Thr	Ser	Ile	His	Val	
302			825					830				835					
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305	Val	Val	Phe	Ser	Leu	Glu	Glu	Pro	Tyr	Glu	Ile	Gln	Leu	Asn	Pro	Val	
306		840					845				850						
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309	Ile	Phe	Trp	Leu	Ser	Phe	Leu	Lys	Ser	Leu	Val	Pro	Val	Glu	Glu	Pro	
310	855					860					865				870		
312	ata	gcc	ttc	ggt	ggc	aag	ctg	aag	aac	cca	ctc	caa	gtt	gtc	ctg	gtg	2994
313	Ile	Ala	Phe	Gly	Gly	Lys	Leu	Lys	Asn	Pro	Leu	Gln	Val	Val	Leu	Val	
314				875						880				885			
316	gcc	acc	cac	gct	gac	atc	atg	aat	gtt	cct	cga	ccg	gct	gga	ggc	gag	3042
317	Ala	Thr	His	Ala	Asp	Ile	Met	Asn	Val	Pro	Arg	Pro	Ala	Gly	Gly	Glu	
318				890					895				900				
320	ttt	gga	tat	gac	aaa	gac	aca	tcg	ttg	ctg	aaa	gag	att	agg	aac	agg	3090
321	Phe	Gly	Tyr	Asp	Lys	Asp	Thr	Ser	Leu	Leu	Lys	Glu	Ile	Arg	Asn	Arg	
322			905					910				915					
324	ttt	gga	aat	gat	ctt	cac	att	tca	aat	aag	ctg	ttt	gtt	ctg	gat	gct	3138
325	Phe	Gly	Asn	Asp	Leu	His	Ile	Ser	Asn	Lys	Leu	Phe	Val	Leu	Asp	Ala	
326		920					925				930						
328	ggg	gct	tct	ggg	tca	aag	gac	atg	aag	gta	ctt	cga	aat	cat	ctg	caa	3186
329	Gly	Ala	Ser	Gly	Ser	Lys	Asp	Met	Lys	Val	Leu	Arg	Asn	His	Leu	Gln	
330	935					940					945				950		
332	gaa	ata	cga	agc	cag	att	gtt	tcg	gtc	tgt	cct	ccc	atg	act	cac	ctg	3234
333	Glu	Ile	Arg	Ser	Gln	Ile	Val	Ser	Val	Cys	Pro	Pro	Met	Thr	His	Leu	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/045,400

DATE: 02/05/2002

TIME: 17:06:01

Input Set : A:\ES.txt

Output Set: N:\CRF3\02052002\J045400.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:39 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3